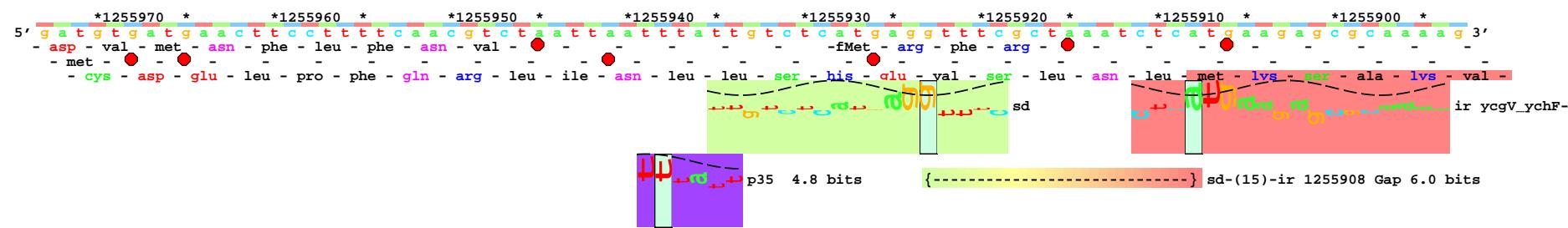


- 1 -
piece 1, NC_000913, ycgV_ychF-, config: linear, direction: -, begin: 1255973, end: 1255156

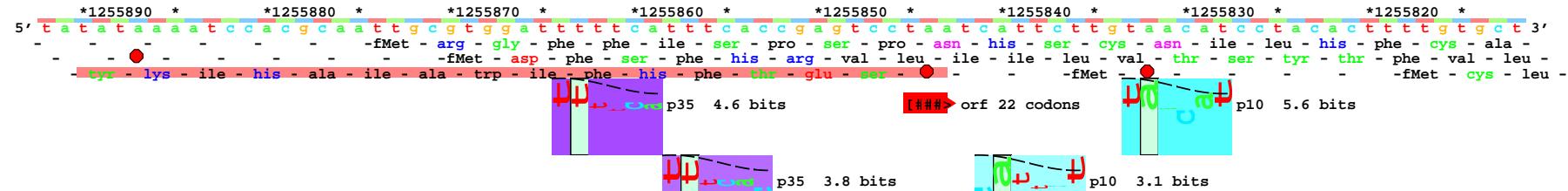


| -----| sd-ir 1255908 ycgV_ychF- total 5.5 bits

p10 1.4 bits

{ p35-(23)-p10 1255915 Gap 1.4 bits

p35-p10 1255915 total 4.8 bits

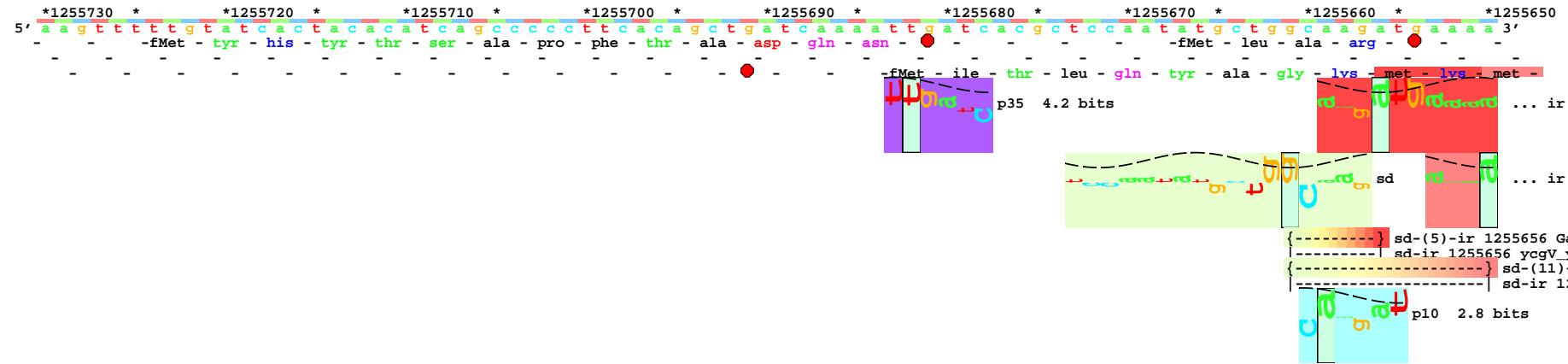
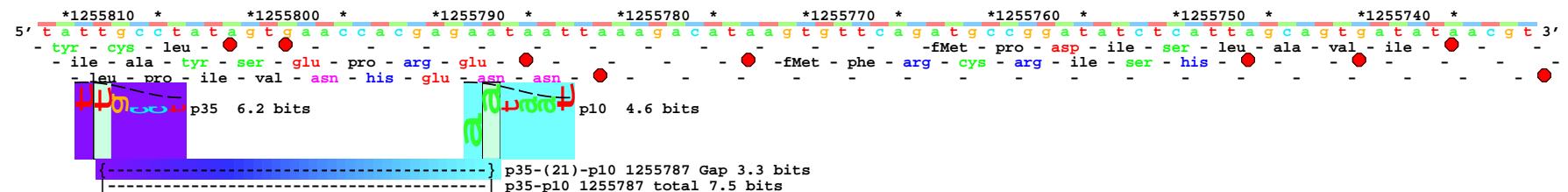


{ p35-(23)-p10 1255840 Gap 1.4 bits

p35-p10 1255840 total 6.3 bits

{ p35-(25)-p10 1255832 Gap 4.0 bits

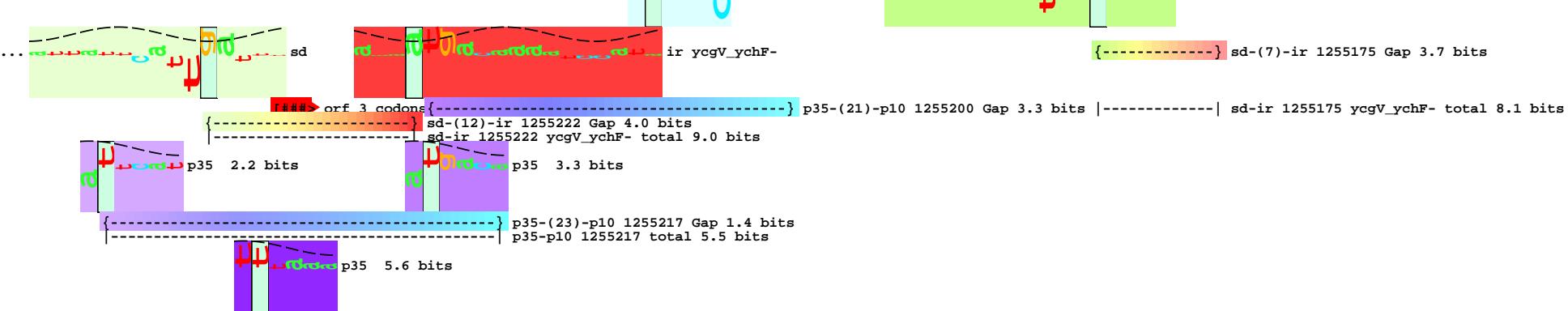
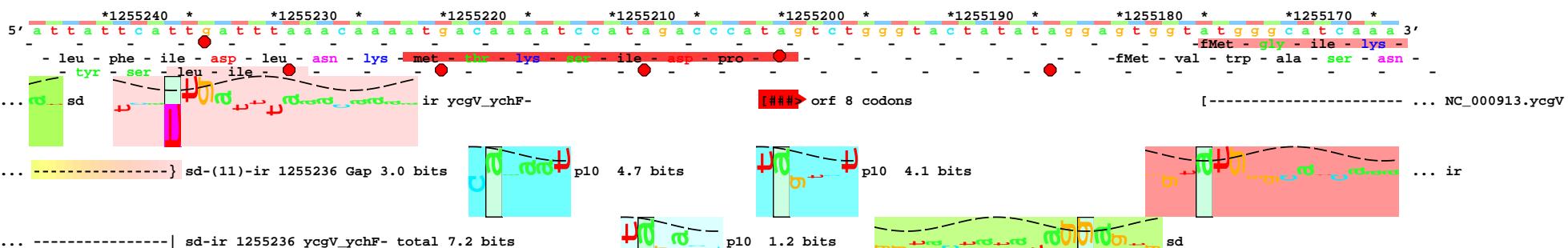
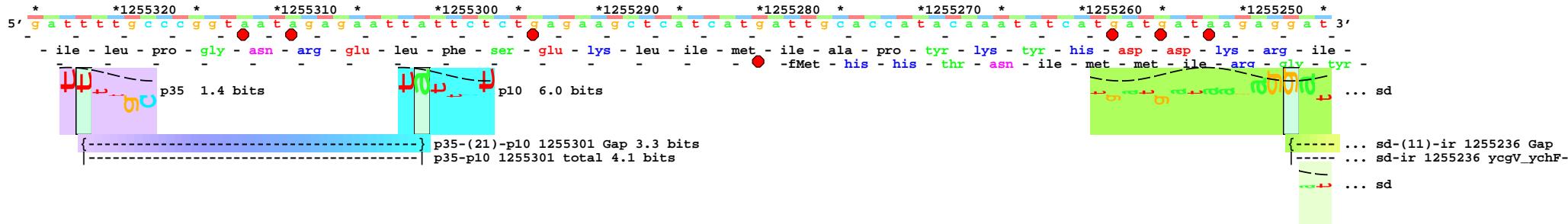
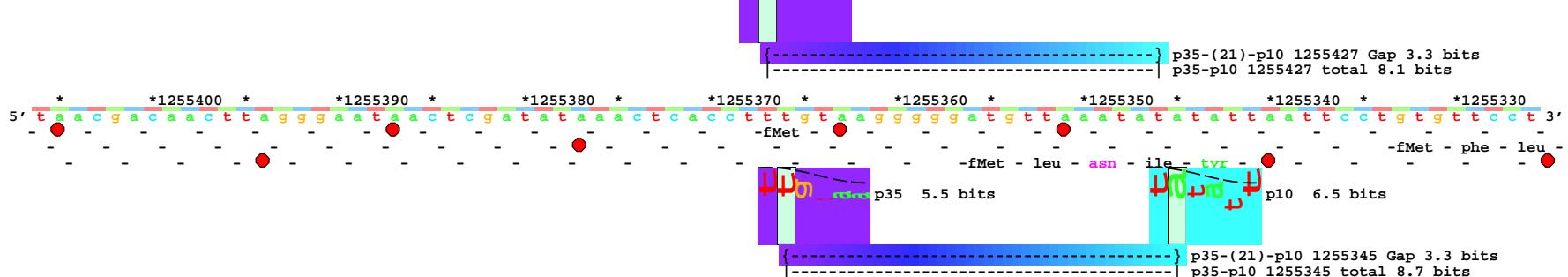
p35-p10 1255832 total 5.3 bits





{...} p35-(23)-p10 1255442 Gap 1.4 bits
p35-p10 1255442 total 7.6 bits

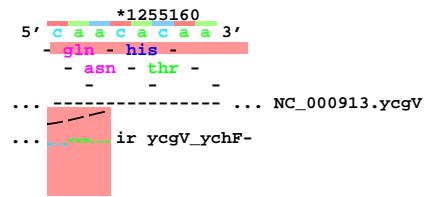
p35 5.5 bits



- 4 -

```
{-----} p35-(23)-p10 1255208 Gap 1.4 bits
|-----| p35-p10 1255208 total 5.3 bits
|-----| p35-p10 1255200 total 4.2 bits
```

*1255160
5' c a a c a c a 3'
- gln - his -
- asn - thr -
... NC_000913.ycgV
... ir ycgV_ychF-



The diagram shows a sequence alignment between two strands. The top strand is labeled '5' and has a sequence of 'c a a c a c a'. Above the sequence is the identifier '*1255160'. Below the sequence, several mutations are indicated: 'gln' at position 1, 'his' at position 2, 'asn' at position 3, and 'thr' at position 4. The bottom strand is labeled '3' and has a sequence of 'ir ycgV_ychF-'. A red shaded rectangular box covers the first four positions of the bottom strand, corresponding to the mutations in the top strand.